

1
SEQUENCE LISTING

5 <110> Regents of the University of Minnesota et al.

<120> Streptococcal C5a peptidase vaccine

<130> 600.450W01

10 <150> US 09/206,898

<151> 1998-12-07

<150> US 08/589,756

<151> 1996-01-22

15 <160> 23

<170> FastSEQ for Windows Version 3.0

20 <210> 1

<211> 1164

<212> PRT

<213> Streptococcus pyogenes

25 <400> 1

Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu

1 5 10 15

Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn

20 25 30

30 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Thr Pro

35 40 45

Gln Pro Thr Thr Val Ser Glu Glu Val Pro Ser Ser Lys Glu Thr Lys

50 55 60

Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Val Ala Asp Asp Ala

35 65 70 75 80

Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Pro Asp Thr Ser Ala

85 90 95

Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys

100 105 110

40 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val

115 120 125

Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
 130 135 140
 Lys Ala Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
 145 150 155 160
 5 Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
 165 170 175
 Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
 180 185 190
 His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
 195 200 205
 10 Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
 210 215 220
 Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
 225 230 235 240
 15 Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val
 245 250 255
 Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
 260 265 270
 Asp Glu Thr Lys Lys Pro Phe Val Tyr Ala Lys Ser Lys Gly Val Arg
 275 280 285
 20 Ile Val Thr Thr Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
 290 295 300
 Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
 305 310 315 320
 25 Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Asn Gln
 325 330 335
 Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu
 340 345 350
 Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
 355 360 365
 30 Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val
 370 375 380
 Lys Gly Lys Ile Ala Leu Ile Glu Arg Ser Asp Ile Asp Phe Thr Asp
 385 390 395 400
 35 Lys Ile Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
 405 410 415
 Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
 420 425 430
 Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
 440 445

Thr Ile Ile Asn Val Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
 770 775 780
 Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
 785 790 795 800
 5 Gln Asp Asp Asp Arg His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
 805 810 815
 Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
 820 825 830
 Gln Phe His Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
 10 835 840 845
 Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
 850 855 860
 Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
 865 870 875 880
 15 Thr Arg Phe Glu Ile Ser Arg Trp Asp Gly Lys Asp Lys Asp Ala Lys
 885 890 895
 Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
 900 905 910
 Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
 20 915 920 925
 Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
 930 935 940
 Arg Arg Leu Thr Leu Ala Ser Lys Pro Gln Thr Ser Gln Pro Val Tyr
 945 950 955 960
 25 Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
 965 970 975
 Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
 980 985 990
 Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
 30 995 1000 1005
 Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
 1010 1015 1020
 Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser
 1025 1030 1035 1040
 35 Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp Gly
 1045 1050 1055
 Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Gly Gln Asp
 1060 1065 1070
 Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Lys
 40 1075 1080 1085

[illegible]

180 185 190
 His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
 195 200 205
 Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
 5 210 215 220
 Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
 225 230 235 240
 Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val
 245 250 255
 10 Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
 260 265 270
 Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
 275 280 285
 Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
 15 290 295 300
 Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
 305 310 315 320
 Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
 325 330 335
 20 Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu
 340 345 350
 Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
 355 360 365
 Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val
 25 370 375 380
 Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp
 385 390 395 400
 Lys Val Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
 405 410 415
 30 Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
 420 425 430
 Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Lys Asp
 435 440 445
 Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
 35 450 455 460
 Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
 465 470 475 480
 Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
 485 490 495
 40 Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser

500 505 510
 Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
 515 520 525
 Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu
 5 530 535 540
 Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
 545 550 555 560
 Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
 565 570 575
 10 Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
 580 585 590
 Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
 595 600 605
 Thr Val Thr Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr
 15 610 615 620
 Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
 625 630 635 640
 Ala Pro Lys Val Leu Tyr Glu Ala Ser Trp Gln Lys Ile Thr Ile Pro
 645 650 655
 20 Ala Asn Ser Ser Lys Gln Val Thr Val Pro Ile Asp Ala Ser Arg Phe
 660 665 670
 Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
 675 680 685
 Phe Val Arg Phe Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile
 25 690 695 700
 Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Val Glu
 705 710 715 720
 Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala
 725 730 735
 30 Asn Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
 740 745 750
 Ala Leu Lys Asn Asn Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
 755 760 765
 Thr Ile Ile Lys Ala Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
 35 770 775 780
 Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
 785 790 795 800
 Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Glu
 805 810 815
 40 Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val

	Gln	Phe	Gln	Gly	Thr	Phe	Leu	Arg	Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu			
	820							825						830					
										835						840		845	
	Val	Leu	Asp	Lys	Glu	Gly	Asn	Val	Val	Trp	Thr	Ser	Glu	Val	Thr	Glu			
5	850							855					860						
	Gln	Val	Val	Lys	Asn	Tyr	Asn	Asn	Asp	Leu	Ala	Ser	Thr	Leu	Gly	Ser			
	865									870			875				880		
	Thr	Arg	Phe	Glu	Lys	Thr	Arg	Trp	Asp	Gly	Lys	Asp	Lys	Asp	Gly	Lys			
	885									890					895				
10	Val	Val	Ala	Asn	Gly	Thr	Tyr	Thr	Tyr	Arg	Val	Arg	Tyr	Thr	Pro	Ile			
	900									905					910				
	Ser	Ser	Gly	Ala	Lys	Glu	Gln	His	Thr	Asp	Phe	Asp	Val	Ile	Val	Asp			
	915									920			925						
	Asn	Thr	Thr	Pro	Glu	Val	Ala	Thr	Ser	Ala	Thr	Phe	Ser	Thr	Glu	Asp			
15	930							935					940						
	Arg	Arg	Leu	Thr	Leu	Ala	Ser	Lys	Pro	Lys	Thr	Ser	Gln	Pro	Val	Tyr			
	945									950			955				960		
	Arg	Glu	Arg	Ile	Ala	Tyr	Thr	Tyr	Met	Asp	Glu	Asp	Leu	Pro	Thr	Thr			
	965									970					975				
20	Glu	Tyr	Ile	Ser	Pro	Asn	Glu	Asp	Gly	Thr	Phe	Thr	Leu	Pro	Glu	Glu			
	980									985					990				
	Ala	Glu	Thr	Met	Glu	Gly	Ala	Thr	Val	Pro	Leu	Lys	Met	Ser	Asp	Phe			
	995									1000					1005				
	Thr	Tyr	Val	Val	Glu	Asp	Met	Ala	Gly	Asn	Ile	Thr	Tyr	Thr	Pro	Val			
25	1010							1015					1020						
	Thr	Lys	Leu	Leu	Glu	Gly	His	Ser	Asn	Lys	Pro	Glu	Gln	Asp	Gly	Ser			
	1025									1030			1035				1040		
	Gly	Gln	Thr	Pro	Asp	Lys	Lys	Pro	Glu	Ala	Lys	Pro	Glu	Gln	Asp	Gly			
	1045									1050					1055				
30	Ser	Asp	Gln	Ala	Pro	Asp	Lys	Lys	Pro	Glu	Ala	Lys	Pro	Glu	Gln	Asp			
	1060									1065					1070				
	Gly	Ser	Gly	Gln	Thr	Pro	Asp	Lys	Lys	Pro	Glu	Thr	Lys	Pro	Glu	Lys			
	1075									1080			1085						
	Asp	Ser	Ser	Gly	Gln	Thr	Pro	Gly	Lys	Thr	Pro	Gln	Lys	Gly	Gln	Pro			
35	1090							1095					1100						
	Ser	Arg	Thr	Leu	Glu	Lys	Arg	Ser	Ser	Lys	Arg	Ala	Leu	Ala	Thr	Lys			
	1105									1110			1115				1120		
	Ala	Ser	Thr	Arg	Asp	Gln	Leu	Pro	Thr	Thr	Asn	Asp	Lys	Asp	Thr	Asn			
	1125									1130					1135				
40	Arg	Leu	His	Leu	Leu	Lys	Leu	Val	Met	Thr	Thr	Phe	Phe	Phe	Gly	Leu			

1140 1145 1150
 Val Ala His Ile Phe Lys Thr Lys Arg Gln Lys Glu Thr Lys Lys
 1155 1160 1165
 5 <210> 3
 <211> 1150
 <212> PRT
 <213> Streptococcus agalactiae
 10 <400> 3
 Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
 1 5 10 15
 Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
 20 25 30
 15 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Thr Val Glu Thr Pro
 35 40 45
 Gln Pro Thr Ala Val Ser Glu Glu Ala Pro Ser Ser Lys Glu Thr Lys
 50 55 60
 Thr Pro Gln Thr Pro Ser Asp Ala Gly Glu Thr Val Ala Asp Asp Ala
 20 65 70 75 80
 Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
 85 90 95
 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
 100 105 110
 25 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
 115 120 125
 Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
 130 135 140
 Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
 30 145 150 155 160
 Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
 165 170 175
 Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
 180 185 190
 35 His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
 195 200 205
 Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
 210 215 220
 Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
 40 225 230 235 240

10

Asn Tyr Ala Gln Ala Ile Arg Asp Ala Ile Asn Leu Gly Ala Lys Val
 245 250 255
 Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
 260 265 270
 5 Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
 275 280 285
 Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
 290 295 300
 Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
 10 305 310 315 320
 Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
 325 330 335
 Leu Thr Glu Thr Val Arg Val Lys Thr Ala Asp Gln Gln Asp Lys Glu
 340 345 350
 15 Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
 355 360 365
 Tyr Ala Tyr Ala Asn Arg Gly Thr Lys Glu Asp Asp Phe Lys Asp Val
 370 375 380
 Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp
 20 385 390 395 400
 Lys Ile Ala Lys Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
 405 410 415
 Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
 420 425 430
 25 Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
 435 440 445
 Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
 450 455 460
 Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
 30 465 470 475 480
 Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
 485 490 495
 Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
 500 505 510
 35 Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
 515 520 525
 Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu
 530 535 540
 Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
 40 545 550 555 560

Figure 1 consists of 12 histograms arranged in a single row. Each histogram represents the distribution of the number of non-zero elements in the vector x for a specific value of n . The x-axis for all histograms is labeled 'x' and ranges from 0 to 120. The y-axis is labeled 'count' and ranges from 0 to 100. The histograms are for $n = 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120$. As n increases, the distribution becomes more concentrated around $n/2$, and the peak count increases.

The diagram illustrates the experimental setup for measuring the time delay of a quantum state. It shows a sequence of operations: an input state $|\psi\rangle$, followed by a Hadamard gate (H), a phase shift gate (ϕ), another Hadamard gate (H), and finally a measurement. The output is a probability distribution P . The diagram is labeled with 'Hadamard gate' and 'Phase shift gate'.

The diagram illustrates the experimental setup for studying the effect of a magnetic field on dendrite growth. It shows a cylindrical sample with a central hole. A magnetic field B is applied along the axis of the cylinder. A current I is applied to the sample, creating a magnetic field B . The sample is surrounded by a fluid medium. The diagram is labeled with various parameters: B , I , and a coordinate system (x, y, z) .

The diagram illustrates the experimental setup for studying the effect of a magnetic field on dendrite growth. It shows a cylindrical sample with a central hole. A magnetic field B is applied along the axis of the cylinder. A current I is applied to the sample, creating a magnetic field B . The sample is surrounded by a fluid medium. The diagram is labeled with various parameters: B , I , and a coordinate system (x, y, z) .

13

<400> 4
gggggggaat tcgtagcggg tatcatggga c 31

<210> 5
5 <211> 31
<212> DNA
<213> Streptococcus pyogenes

<400> 5
10 gggggggaat tcgggtgctg caatatctgg c 31

<210> 6
<211> 17
<212> DNA
15 <213> Streptococcus pyogenes

<400> 6
gtaaaacgac ggccagt 17

<210> 7
20 <211> 19
<212> DNA
<213> Streptococcus pyogenes

<400> 7
25 aaggacgaca cattgcgta 19

<210> 8
<211> 31
30 <212> DNA
<213> Streptococcus pyogenes

<400> 8
ccccccggat ccacaaaaac cccacaaaact c 31

35 <210> 9
<211> 18
<212> DNA
<213> Streptococcus pyogenes

40

14

<400> 9
gagtggccct ccaatagc 18

<210> 10
5 <211> 35
<212> DNA
<213> Streptococcus pyogenes

<400> 10
10 ccccccgat ccaatactgt gacagaagac actcc 35

<210> 11
<211> 25
<212> DNA
15 <213> Streptococcus pyogenes

<400> 11
tttctggaac tagtatgtct gcgcc 25

<210> 12
20 <211> 41
<212> DNA
<213> Streptococcus pyogenes

<400> 12
25 cccccctcg agatgtaaac gatttgatc cttgtcatta g 41

<210> 13
<211> 25
30 <212> DNA
<213> Streptococcus pyogenes

<400> 13
cagtgattga tgctggtttt gataa 25

35
<210> 14
<211> 18
<212> DNA
<213> Streptococcus pyogenes

40

15

<400> 14
agctactatc agcaccag 18

<210> 15
5 <211> 38
<212> DNA
<213> Streptococcus pyogenes

<400> 15
10 ccccccgaat tcattactgt gacagaagac actcctgc 38

<210> 16
<211> 39
<212> DNA
15 <213> Streptococcus pyogenes

<400> 16
ccccccggat ccttattgtt ctggtttatt agagtggcc 39

<210> 17
20 <211> 33
<212> DNA
<213> Streptococcus pyogenes

<400> 17
25 attgctgctg gttttgataa aaatcatgaa gcg 33

<210> 18
<211> 18
30 <212> DNA
<213> Streptococcus pyogenes

<400> 18
cactgcaaca acagtccc 18

35
<210> 19
<211> 18
<212> DNA
<213> Streptococcus pyogenes

40

S

[illegible]

	370						375					380							
	Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu	Arg	Gly	Asp	Ile	Asp	Phe	Lys	Asp			
	385						390					395						400	
	Lys	Ile	Ala	Asn	Ala	Lys	Lys	Ala	Gly	Ala	Val	Gly	Val	Leu	Ile	Tyr			
5							405					410						415	
	Asp	Asn	Gln	Asp	Lys	Gly	Phe	Pro	Ile	Glu	Leu	Pro	Asn	Val	Asp	Gln			
	420						425					430							
	Met	Pro	Ala	Ala	Phe	Ile	Ser	Arg	Lys	Asp	Gly	Leu	Leu	Lys	Glu				
	435						440					445							
10	Asn	Pro	Gln	Lys	Thr	Ile	Thr	Phe	Asn	Ala	Thr	Pro	Lys	Val	Leu	Pro			
	450						455					460							
	Thr	Ala	Ser	Gly	Thr	Lys	Leu	Ser	Arg	Phe	Ser	Ser	Trp	Gly	Leu	Thr			
	465						470					475						480	
	Ala	Asp	Gly	Asn	Ile	Lys	Pro	Asp	Ile	Ala	Ala	Pro	Gly	Gln	Asp	Ile			
15	485						490					495							
	Leu	Ser	Ser	Val	Ala	Asn	Asn	Lys	Tyr	Ala	Lys	Leu	Ser	Gly	Thr	Ser			
	500						505					510							
	Met	Ser	Ala	Pro	Leu	Val	Ala	Gly	Ile	Met	Gly	Leu	Leu	Gln	Lys	Gln			
	515						520					525							
20	Tyr	Glu	Thr	Gln	Tyr	Pro	Asp	Met	Thr	Pro	Ser	Glu	Arg	Leu	Asp	Leu			
	530						535					540							
	Ala	Lys	Lys	Val	Leu	Met	Ser	Ser	Ala	Thr	Ala	Leu	Tyr	Asp	Glu	Asp			
	545						550					555						560	
	Glu	Lys	Ala	Tyr	Phe	Ser	Pro	Arg	Gln	Gln	Gly	Ala	Gly	Ala	Val	Asp			
25	565						570					575							
	Ala	Lys	Lys	Ala	Ser	Ala	Ala	Thr	Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn			
	580						585					590							
	Thr	Ser	Ser	Lys	Val	His	Leu	Asn	Asn	Val	Ser	Asp	Lys	Phe	Glu	Val			
	595						600					605							
30	Thr	Val	Thr	Val	His	Asn	Lys	Ser	Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr			
	610						615					620							
	Gln	Ala	Thr	Val	Gln	Thr	Asp	Lys	Val	Asp	Gly	Lys	Leu	Phe	Ala	Leu			
	625						630					635						640	
	Ala	Pro	Lys	Ala	Leu	Tyr	Glu	Ala	Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro			
35	645						650					655							
	Ala	Asn	Ser	Ser	Lys	Gln	Val	Thr	Ile	Pro	Ile	Asp	Val	Ser	Gln	Phe			
	660						665					670							
	Ser	Lys	Asp	Leu	Leu	Ala	Pro	Met	Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly			
	675						680					685							
40	Phe	Val	Arg	Phe	Lys	Gln	Asp	Pro	Thr	Lys	Glu	Glu	Leu	Met	Ser	Ile			

690 695 700
 Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
 705 710 715 720
 Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala
 5 725 730 735
 Asn Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
 740 745 750
 Ala Leu Lys Asn Asn Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
 755 760 765
 10 Thr Ile Ile Lys Ala Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
 770 775 780
 Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
 785 790 795 800
 Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
 15 805 810 815
 Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
 820 825 830
 Gln Phe Gln Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
 835 840 845
 20 Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
 850 855 860
 Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
 865 870 875 880
 Thr Arg Phe Glu Lys Thr Arg Trp Asp Gly Lys Asp Lys Asp Gly Lys
 25 885 890 895
 Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
 900 905 910
 Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
 915 920 925
 30 Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
 930 935 940
 Arg Arg Leu Thr Leu Ala Ser Lys Pro Lys Thr Ser Gln Pro Val Tyr
 945 950 955 960
 Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
 35 965 970 975
 Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
 980 985 990
 Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
 995 1000 1005
 40 Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val

20

	1010		1015		1020
	Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser				
	1025		1030		1035
	Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp Gly				
5			1045		1050
	Ser Gly Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp				
			1060		1065
					1070
	Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln				
			1075		1080
					1085
10	Asp Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu				
			1090		1095
					1100
	Lys Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln				
			1105		1110
					1115
	Pro Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr				
15			1125		1130
					1135
	Lys Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr				
			1140		1145
					1150
	Asn Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Leu Gly				
			1155		1160
					1165
20	Leu Val Ala His Ile Phe Lys Thr Lys Arg Thr Lys Lys				
			1170		1175
					1180